



10830118.txt  
SEQUENCE LISTING

<110> GUERIN-MARCHAND, CLAUDINE  
DRUILHE, PIERRE

<120> DNA SEQUENCES ENCODING PEPTIDE SEQUENCES SPECIFIC FOR  
THE HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES  
CAPABLE OF STIMULATING THE T LYMPHOCYTES (as amended)

<130> 010830-118

<140> 09/900,963

<141> 2001-07-10

<150> 08/098,327

<151> 1993-11-24

<150> PCT/FR92/00104

<151> 1992-02-05

<150> FR 91 01286

<151> 1991-02-05

<160> 47

<170> PatentIn Ver. 3.3

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Arg

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Leu

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Xaa

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Gln

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Glu

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Leu

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Xaa

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                   20                  25                  30  
 Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr Ile Pro His Gln Ser  
                   35                  40                  45  
 Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg Asp Ser Lys Glu Ile  
           50                  55                  60  
 Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile Thr Thr Asn Val Glu  
           65                  70                  75                  80  
 Gly Arg Arg Asp Ile His Lys Gly His Leu Glu Glu Lys Lys Asp Gly  
                   85                  90                  95  
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           100                  105

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 Leu Tyr Gly Arg Leu Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn  
 35 40 45  
 Glu Arg Gly Tyr Tyr Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn  
 50 55 60  
 Arg Gly Asn Ser Arg Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr  
 65 70 75 80  
 Asn Arg Glu Ser Ile Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His  
 85 90 95  
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 100 105 110  
 Lys Glu Asp Lys Ser  
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<213> Plasmodium falciparum

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Asp Thr Lys Lys Asn Leu Glu Arg Lys Lys Glu His Gly Asp Ile Leu  
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Asn Ser Arg Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg  
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20

25

30

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 Phe Asn Ser Leu Val Lys Ser Val Gln Gln Glu Gln Gln His Asn Val  
 35 40 45  
 Glu Glu Lys Val Glu Glu Ser Val Glu Glu Asn Asp Glu Glu Ser Val  
 50 55 60  
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 65 70 75 80  
 Ala Ser Ser Val Glu Glu Ser Ile Ala Ser Ser Val Asp Glu Ser Ile  
 85 90 95  
 Asp Ser Ser Ile Glu Glu Asn Val Ala Pro Thr Val Glu Glu Ile Val  
 100 105 110  
 Ala Pro Thr Val Glu Glu Ile Val Ala Pro Ser Val Val Glu Lys Cys  
 115 120 125  
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 145 150

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 35 40 45

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1 5 10 15  
 Val Lys Glu Asn Ile Leu Glu Glu Ser Gln  
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 20 25

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 Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln  
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20 25 30  
Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln  
35 40 45  
Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu  
50 55 60  
Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys  
65 70 75 80  
Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu  
85 90 95  
Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys  
100 105 110  
Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala  
115 120 125  
Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu  
130 135 140  
Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg  
145 150 155 160  
Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu  
165 170 175  
Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln  
180 185 190  
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195 200 205  
Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg Lys Lys Glu His  
210 215 220  
Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu Glu Ile Pro Ala  
225 230 235 240  
Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr Ile Pro His Gln  
245 250 255  
Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg Asp Ser Lys Glu  
260 265 270  
Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile Thr Thr Asn Val  
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Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu Glu Lys Lys Asp  
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ctaaagaaaa gttgcaagaa caacaaagcg attttagaaca agagagacgt gctaaagaaa 240
agttgcaaga acaacaaagc gatttagaac aagatagact tgctaaagaa aagttacaag 300
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aagaaaagtt gcaagaacaa caaagcgatt tagaacaaga gagacgtgct aaagaaaagt 600
tgcaagagca gcaaagagat ttagaacaaca ggaaggctga tacgaaaaaa aatttagaaa 660
gaaaaaagga acatggagat atattagcag aggtttata tggctcgttta gaaataccag 720
ctatagaact tccatcagaa aatgaacgtg gatattatat accacatcaa tcttctttac 780
ctcaggacaa cagagggaat agtagagatt ccaaggaaat atctataata gaaaaaacia 840
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aatgacgaag aaagtgtaga agaaaatgta gaagaaaatg tagaagaaaa tgacgacgga 240
agtgtagcct caagtgttga agaaagtata gcttcaagtg ttgatgaaag tatagattca 300
agtattgaag aaaatgtagc tccaactgtt gaagaaatcg tagctccaac tgttgaagaa 360
attgtagctc caagtgttgt agaaaagtgt gctccaagtg ttgaagaaag tgtagctcca 420
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ctaaagaaaa gttgcaagaa caacaaagcg attttagaaca agagagacgt gctaaagaaa 960
ggttgcagaa acaacaaagc gatttaga 988

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ttg ata ttt cat ata aat gga aag ata ata aag aat tct gaa aaa gat 96  
 Leu Ile Phe His Ile Asn Gly Lys Ile Ile Lys Asn Ser Glu Lys Asp  
 20 25 30

gaa atc ata aaa tct aac ttg aga agt ggt tct tca aat tct agg aat 144  
 Glu Ile Ile Lys Ser Asn Leu Arg Ser Gly Ser Ser Asn Ser Arg Asn  
 35 40 45

cga ata aat gag gaa aat cac gag aag aaa cac gtt tta tct cat aat 192  
 Arg Ile Asn Glu Glu Asn His Glu Lys Lys His Val Leu Ser His Asn  
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tca tat gag aaa act aaa aat aat gaa aat aat aaa ttt ttc gat aag 240  
 Ser Tyr Glu Lys Thr Lys Asn Asn Glu Asn Asn Lys Phe Phe Asp Lys  
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gat aaa gag tta acg atg tct aat gta aaa aat gtg tca caa aca aat 288  
 Asp Lys Glu Leu Thr Met Ser Asn Val Lys Asn Val Ser Gln Thr Asn  
 85 90 95

ttc aaa agt ctt tta aga aat ctt ggt gtt tca gag aat ata ttc ctt 336  
 Phe Lys Ser Leu Leu Arg Asn Leu Gly Val Ser Glu Asn Ile Phe Leu  
 100 105 110

aaa gaa aat aaa tta aat aag gaa ggg aaa tta att gaa cac ata ata 384  
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 115 120 125

aat gat gat gac gat aaa aaa aaa tat att aaa ggg caa gac gaa aac 432  
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 130 135 140

aga caa gaa gat ctt gaa gaa aaa gca gct aaa gaa aag tta cag ggg 480  
 Arg Gln Glu Asp Leu Glu Glu Lys Ala Ala Lys Glu Lys Leu Gln Gly  
 145 150 155 160

caa caa agc gat tca gaa caa gag aga cgt gct aaa gaa aag ttg caa 528  
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10830118.txt

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                   20                  25                  30  
 Glu Ile Ile Lys Ser Asn Leu Arg Ser Gly Ser Ser Asn Ser Arg Asn  
                   35                  40                  45  
 Arg Ile Asn Glu Glu Asn His Glu Lys Lys His Val Leu Ser His Asn  
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 Ser Tyr Glu Lys Thr Lys Asn Asn Glu Asn Asn Lys Phe Phe Asp Lys  
   65                  70                  75                  80  
 Asp Lys Glu Leu Thr Met Ser Asn Val Lys Asn Val Ser Gln Thr Asn  
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Phe Lys Ser Leu Leu Arg Asn Leu Gly Val Ser Glu Asn Ile Phe Leu  
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 Lys Glu Asn Lys Leu Asn Lys Glu Gly Lys Leu Ile Glu His Ile Ile  
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 Arg Gln Glu Asp Leu Glu Glu Lys Ala Ala Lys Glu Lys Leu Gln Gly  
 145 150 155 160  
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 195 200 205  
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 225 230 235 240  
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 260 265 270  
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 275 280 285  
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&lt;212&gt; DNA

&lt;213&gt; Plasmodium falciparum

&lt;400&gt; 39

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ataccagcta	tagaacttcc	atcagaaaat	gaacgtggat	attatatacc	acatcaatct	780
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10830118.txt

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aaaacaaata gagaatctat tacaacaaat gttgaaggac gaagggatat acataaagga 900
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gatttagatg aaggaataga aaaatcatca gaagaattat ctgaagaaaa aataaaaaaa 1260
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gatgagcata ttaaaaaata taaaaatgat aagcaggtta ataaggaaaa ggaaaaattc 1380
ataaaatcat tgtttcatat atttgacgga gacaatgaaa ttttacagat cgtggatgag 1440
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ttg caa gaa caa caa agc gat tta gaa caa gat aga ctt gct aaa gaa 96  
 Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu  
 20 25 30

aag tta caa gag cag caa agc gat tta gaa caa gag aga ctt gct aaa 144  
 Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys  
 35 40 45

gaa aag ttg caa gaa caa caa agc gat cta gaa caa gag aga cgt gct 192  
 Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala  
 50 55 60

aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt 240  
 Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg  
 65 70 75 80

gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gat aga 288  
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 85 90 95

ctt gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gag 336  
 Page 20

## 10830118.txt

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Arg	Asp	Leu	Glu	Gln	Arg	Lys	Ala	Asp	Thr	Lys	Lys	Asn	Leu	Glu	Arg	
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Ile	Pro	His	Gln	Ser	Ser	Leu	Pro	Gln	Asp	Asn	Arg	Gly	Asn	Ser	Arg	
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Thr	Thr	Asn	Val	Glu	Gly	Arg	Arg	Asp	Ile	His	Lys	Gly	His	Leu	Glu	
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Glu	Lys	Lys	Asp	Gly	Ser	Ile	Lys	Pro	Glu	Gln	Lys	Glu	Asp	Lys	Ser	
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gct	gac	ata	caa	aat	cat	aca	tta	gag	aca	gta	aat	att	tct	gat	gtt	1008
Ala	Asp	Ile	Gln	Asn	His	Thr	Leu	Glu	Thr	Val	Asn	Ile	Ser	Asp	Val	
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aat	gat	ttt	caa	ata	agt	aag	tat	gag	gat	gaa	ata	agt	gct	gaa	tat	1056
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## 10830118.txt

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gga Gly 385	att Ile	tat Tyr	aaa Lys	gaa Glu	cta Leu 390	gaa Glu	gat Asp	ttg Leu	ata Ile	gag Glu 395	aaa Lys	aat Asn	gaa Glu	aat Asn	tta Leu 400	1200
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gaa Glu	aaa Lys	ata Ile	aaa Lys 420	aaa Lys	gga Gly	aag Lys	aaa Lys	tat Tyr 425	gaa Glu	aaa Lys	aca Thr	aag Lys	gat Asp 430	aat Asn	aat Asn	1296
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aaa Lys	aat Asn 450	gat Asp	aag Lys	cag Gln	gtt Val	aat Asn 455	aag Lys	gaa Glu	aag Lys	gaa Glu	aaa Lys 460	ttc Phe	ata Ile	aaa Lys	tca Ser	1392
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## 10830118.txt

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## 10830118.txt

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 35 40 45  
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 65 70 75 80  
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 85 90 95



## 10830118.txt

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Leu	Glu	Gln	Glu	Arg	Arg	Ala	Lys	Glu	Lys	Leu	Gln	Glu	Gln	Gln	Ser	
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Asp	Leu	Glu	Gln	Glu	Arg	Arg	Ala	Lys	Glu	Lys	Leu	Gln	Glu	Gln	Gln	
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Asp	Ser	Lys	Glu	Ile	Ser	Ile	Ile	Glu	Lys	Thr	Asn	Arg	Glu	Ser	Ile	
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gga Gly 385	att Ile	tat Tyr	aaa Lys	gaa Glu	cta Leu 390	gaa Glu	gat Asp	ttg Leu	ata Ile	gag Glu 395	aaa Lys	aat Asn	gaa Glu	aat Asn	tta Leu 400	1200
gat Asp	gat Asp	tta Leu	gat Asp	gaa Glu 405	gga Gly	ata Ile	gaa Glu	aaa Lys	tca Ser 410	tca Ser	gaa Glu	gaa Glu	tta Leu	tct Ser 415	gaa Glu	1248
gaa Glu	aaa Lys	ata Ile	aaa Lys 420	aaa Lys	gga Gly	aag Lys	aaa Lys	tat Tyr 425	gaa Glu	aaa Lys	aca Thr	aag Lys	gat Asp 430	aat Asn	aat Asn	1296
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ttg Leu 465	ttt Phe	cat His	ata Ile	ttt Phe	gac Asp 470	gga Gly	gac Asp	aat Asn	gaa Glu	att Ile 475	tta Leu	cag Gln	atc Ile	gtg Val	gat Asp 480	1440
gag Glu	tta Leu	tct Ser	gaa Glu	gat Asp 485	ata Ile	act Thr	aaa Lys	tat Tyr	ttt Phe 490	atg Met	aaa Lys	cta Leu	taa	aag	gtt	1488
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 Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys  
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 Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala  
 50 55 60  
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 Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg

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 Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser  
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 Glu Leu Ser Glu Asp Ile Thr Lys Tyr Phe Met Lys Leu  
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